



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

PATENT

#9
AP 3/7/01

Application of:

JENNIE BIH-JIEN SHEN

CASE NO.: BB1137

APPLICATION NO.: 09/326,285

GROUP ART UNIT: 1638

FILED: JUNE 7, 1999

EXAMINER: P. BUI

FOR: GENES FOR DESATURASES TO ALTER
LIPID PROFILES IN CORN

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RESPONSE TO RESTRICTION REQUIREMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

This is submitted in response to the Office Action dated January 30, 2001 regarding the above-identified application. Applicants respectfully request reconsideration and submit the following in support thereof.

Remarks

Applicants hereby provisionally elect, with traverse, the subject matter of Group XI, i.e., Claims 151-168 and 171, for further prosecution in the instant application subject to Applicants' right to pursue the nonelected subject matter in a divisional application or applications pursuant to 35 USC §121.

Applicants further provisionally elect one or inventions (i) – (xii), specifically, (vii) * SEQ ID NO: 1 to be examined as a subcombination. To the extent that an election of (a) – (m) is required, then Applicants provisionally elect (c) – SEQ ID NO:39.

Applicants respectfully submit that insofar as (i) – (xii) are concerned, a sequence and its reverse complement are so intricably intertwined as to constitute a single inventive concept. The DNA molecule is a “double helix” – a duplex of entwined antiparallel strands. In each duplex, the bases or nucleotides are “paired” by hydrogen bonds to complementary nucleotides on the other strand.

Specifically, each A is paired with a T and vice versa, and each C is paired with a G and vice versa. The reverse complement of a DNA sequence is formed by reversing the letters, interchanging A and T and interchanging C and G, e.g., the reverse complement of ACCTGAG is CTCAGGT. However, in order to determine the reverse complement, one must know the nucleotide sequence to which the reverse complement is desired.

In the instant invention, the reverse complement of a nucleic acid fragment or subfragment can be used in constructing a chimeric gene designed to express antisense RNA

for all or part of the isolated nucleic acid fragment. (Specification, page 22 at lines 33 – 38). It is believed that no undue burden is created in searching a nucleotide sequence and its reverse complement.

Applicants respectfully request reconsideration of the position that the nucleotide sequences and their reverse complements as set forth on page 4 of the Office Actions constitute separate inventions since it is respectfully submitted that a nucleotide sequence and its reverse complement really do constitute a single inventive concept for all the reasons discussed above.

With respect to (a) – (m), it is noted that these sequences represent various oleosin promoter fragments as discussed in Example 6 on pages 36-41. As is stated on page 36 of the specification, these various fragments were designed to remove a potential negative regulatory element and to determine the optimal length with a high activity without losing its tissue specificity. The results of the promoter deletion assay are presented in Table 2 on page 40. It is respectfully submitted that these are all oleosin promoter fragments of varying lengths. However, the constructs were comparable except for the length of the promoter fragment as is indicated in Table 2 on page 40 of the specification. Given this, it is respectfully submitted that except for the amount of activity these promoter fragments are sufficiently related as to constitute a single inventive concept.

In view of the above discussion, Applicant respectfully requests reconsideration of the restriction requirement with respect to (i) – (xii) and (a) – (m). Please charge any fees associated with the filing of this response to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

Respectfully submitted,

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Dated: February 28, 2001

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